

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run On: August 4, 2003, 15:46:02 ; Search time 18 Seconds
(without alignments)
578.248 Million cell updates/sec

Title: US-09-931-836-2
Perfect score: 1367

Sequence: 1 MLWRLQIYVQLLLAFFLPFC.....LHGHDQRFSTFAGFLLFETK 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:
5: /cgn2_6/ptodata/1/iaa/PCTUS_Comb.pep:
6: /cgn2_6/ptodata/1/iaa/backfiles1..pep:
* Pred. No. is the number of results Predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1367	100.0	246	4 US-09-552-225A-2	Sequence 2, Appli
2	95.9	246	4 US-09-552-225A-12	Sequence 12, Appli	
3	912	42.6	105	3 US-09-188-930-147	Sequence 147, Appli
4	582	42.6	105	3 US-09-188-930-280	Sequence 280, Appli
5	582	42.6	105	4 US-09-312-233C-147	Sequence 147, Appli
6	582	42.6	105	4 US-09-312-233C-280	Sequence 280, Appli
7	319	23.3	285	4 US-09-312-233C-382	Sequence 382, Appli
8	316	23.1	294	3 US-09-388-930-294	Sequence 294, Appli
9	316	23.1	294	4 US-09-312-233C-294	Sequence 294, Appli
10	296.5	21.7	260	4 US-09-481-847-198	Sequence 198, Appli
11	296.5	21.7	287	4 US-09-481-847-349	Sequence 349, Appli
12	294	21.5	244	4 US-09-483-911-2	Sequence 2, Appli
13	294	21.5	247	4 US-09-776-916-4	Sequence 4, Appli
14	294	21.5	247	4 US-09-509-517-4	Sequence 4, Appli
15	293.5	21.5	231	4 US-09-530-123-2	Sequence 2, Appli
16	293.5	21.5	244	3 US-08-463-911-7	Sequence 7, Appli
17	293.5	21.5	244	3 US-09-140-804-3	Sequence 3, Appli
18	293.5	21.5	244	4 US-09-336-336-20	Sequence 20, Appli
19	293.5	21.5	244	4 US-09-330-23-1	Sequence 1, Appli
20	293.5	21.5	244	4 US-09-686-938B-3	Sequence 6, Appli
21	293.5	21.5	244	4 US-09-911-176B-48	Sequence 48, Appli
22	293.5	21.5	244	4 US-09-552-225A-3	Sequence 3, Appli
23	293.5	21.5	244	4 US-09-619-740-51	Sequence 51, Appli
24	293.5	21.5	244	4 US-09-776-916-6	Sequence 6, Appli
25	293.5	21.5	244	4 US-09-909-547-6	Sequence 6, Appli
26	293.5	21.5	244	4 US-09-569-852B-6	Sequence 6, Appli
27	293	21.4	247	4 US-09-776-976-2	Sequence 11, Appli

ALIGMENTS

RESULT 1
DS-09-552-225A-2

; Sequence 2, Application US/09552225A
; Patent No. 651233
; GENERAL INFORMATION:
; APPLICANT: Piddington, Christopher S.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG 2 ACRP3
; FILE REFERENCE: 99-09
; CURRENT APPLICATION NUMBER: US/09-552-225A
; CURRENT FILING DATE: 2000-04-19
; PRIORITY APPLICATION NUMBER: 60/130,199
; PRIORITY FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSDQ for Windows Version 3.0
; SEQ ID NO: 2
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-552-225A-2

Query Match 100.0%; Score 1367; DB 4; Length 246;
Best Local Similarity 100.0%; Pred. No. 6, 6e-130;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLWRLQIYVQLLLAFFLPFCDEYMSPTOTGCLPPDCSKCCHGDYSFRGYQGPGRPG 60
Db 1 MLWRLQIYVQLLLAFFLPFCDEYMSPTOTGCLPPDCSKCCHGDYSFRGYQGPGRPG 60

Qy 61 PPGIPGNHGNNGNATCHEGAKGEKGDKGDGLPGRQRQHQPKGKGKGPQGIPPELQIAF 120
Db 61 PPGIPGNHGNNGNATCHEGAKGEKGDKGDGLPGRQRQHQPKGKGKGPQGIPPELQIAF 120

Qy 121 MASLATHFSNQNSGIIFFSVENIGNIFEDVMTGREGAPVSSVYEFFSMARKHEDVEVYV 180
Db 121 MASLATHFSNQNSGIIFFSVENIGNIFEDVMTGREGAPVSSVYEFFSMARKHEDVEVYV 180

Qy 181 YLMHNHGNTVFSYNSYEMKGKSQTSSNHAVLKLAKGEDEVLRMNGALHGDIHQRFSTFAGF 240
Db 181 YLMHNHGNTVFSYNSYEMKGKSQTSSNHAVLKLAKGEDEVLRMNGALHGDIHQRFSTFAGF 240

RESULT 2
US-09-552-225A-12
; Sequence 12, Application US/09552225A
; Patent No. 651233